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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=16; hr=8; min=29; sec=11; ms=981;]

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Reviewer Comments:

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

Numeric identifier <160> must reflect the total number of sequences in the sequence listing. There are only 226 sequences in this sequence listing but, <160> states there are 229. Please make all necessary changes

<210> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> VEGFR-1 derived peptides

<400> 129

Lys Leu Leu Arg Gly His Thr Leu Val

Numeric identifier "<211> Length" is mandatory for each SEQ ID number.

SEQUENCE LISTING

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

<170> Patent In version 3.4

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<223> primer

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 <400> 6
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 <210> 8
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21

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<211> 19

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<400> 18

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<210> 19

<211> 147

<212> PRT

<213> Homo Sapiens

<400> 147

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Glu Ile Glu Pro Glu
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
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Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
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Pro Arg Arg

145

<210> 20

<211> 444

<212> DNA

<213> Homo Sapiens

<400> 20

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gtgaagtcca tggatgtcta tcagcgcagc tactgccata caatcgagac cctggtggac 180

atcttccagg agtaccctga tgagatcgag tacatcttca agccatectg tgtgccctg 240
 atgcgatgcg ggggctgctg caatgacgag ggcttgaggt gtgtgccac tgaggagtcc 300
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360
 agcttcttac agcacaacaa atgtgaatgc agaccaaga aagatagagc aagacaagaa 420
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<210> 21
 <211> 147
 <212> PRT
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<400> 147

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 20 25 30
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Ala Ile Ala Pro Ala
 100 105 110
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140
 Pro Arg Arg
 145

<210> 22
 <211> 444
 <212> DNA
 <213> Homo Sapiens

<400> 22

atgaactttc tgetgtcttg ggtgcattgg agcettgect tgetgtctta cctccaccat 60

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 gtgaagttca tggatgtcta tcagcgagc tactgccatc caatcgagac cctgtggac 180
 atcttcagg agtacctga tgagatcgag tacatcttca agccatctg tgtgccctg 240
 atgcgatcgc ggggctgctg caatgacgag ggctggagt gtgtgccac tgaggagtcc 300
 aacatcacca tgcagattat ggcaatgca cctgcacaag gccacacat aggagagatg 360
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 aaatgtgaca agccggaggc gtaa 444

<210> 23
 <211> 314
 <212> PRT
 <213> Homo Sapiens

<400> 314

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Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
 20 25 30

Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
 35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 50 55 60

Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
 65 70 75 80

Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
 85 90 95

Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
 100 105 110

Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125

Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140

Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
 145 150 155 160

Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
 165 170 175

Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile

Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
195 200 205

Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
210 215 220

Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
225 230 235 240

Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
245 250 255

Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
260 265 270

Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
275 280 285

Leu Ser Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu
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Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met
305 310

<210> 24

<211> 943

<212> DNA

<213> Homo Sapiens

<400> 24

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cttacaatta aggetaatac aactcttcaa attacttgca ggggacagag ggaactggac 180

tggctttggc ccaataatca gagtggcagt gagcaaaagg tggaggtgac tgagtgcagc 240

gatggcctct tctgtaagac actcaacaatt ccaaaagtga tcggaatga cactggagcc 300

tacaagtgtc tctaccggga aactgacttg gctcgggta tttatgtcta tgtcaagat 360

tacagatctc catttatgac ttctgttagt gaccaacatg gagtcgtgta cattactgag 420

aacaaaaaca aaactgtggt gattccatgt ctgggtcca ttcaaatct caactgtgca 480

ctttgtgcaa gataccaga aaagagattt gttcctgat gtaacagaat ttctgggac 540

agcaagaagg gctttactat tccagctac atgateagc atgctggcat ggtcttctgt 600

gaagcaaaaa ttaatgatga aagttaccag tctattatgt acatagttgt cgttgtaggg 660

tataggattt atgatgtggt tctgagtcg tctcatgaa ttgaactatc tgttgagaa 720

aagcttgtct taaattgtac agcaagaact gaactaaatg tggggattga ctccaactgg 780
 gaataccctt ctctgaagca tcagcataag aaacttgtaa accgagacct aaaaaccag 840
 tctgggagtg agatgaagaa atttttgagc accttaacta tagatggtgt aaccoggagt 900
 gaccaaggat tgtacacctg tgcagcatcc agtgggctga tga 943

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 <211> 611
 <212> PRI
 <213> Homo sapiens

<400> 611

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Asn Leu Glu Ile Ile Ile Leu Val Gly Thr Ala Val Ile Ala Met Phe
 20 25 30

Phe Trp Leu Leu Leu Val Ile Ile Leu Arg Thr Val Lys Arg Ala Asn
 35 40 45

Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp
 50 55 60

Glu Leu Pro Leu Asp Glu His Cys Glu Arg Leu Pro Tyr Asp Ala Ser
 65 70 75 80

Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly
 85 90 95

Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp
 100 105 110

Lys Thr Ala Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys Glu Gly
 115 120 125

Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu
 130 135 140

Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys
 145 150 155 160

Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys Lys Phe
165 170 175

Gly Asn Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val Pro
180 185 190

Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly
195 200 205

Ala Ile Pro Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser
210 215 220

Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp
225 230 235 240

Val Glu Glu Glu Glu Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr
245 250 255

Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu
260 265 270

Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn
275 280 285

Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu
290 295 300

Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala
305 310 315 320

Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val
325 330 335

Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
340 345 350

Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu
355 360 365

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp
370 375 380

Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly

385	390	395	400
Glu Pro Ser Gln Arg Pro Thr Phe Ser Glu Leu Val Glu His Leu Gly			
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Asn Leu Leu Gln Ala Asn Ala Gln Gln Asp Gly Lys Asp Tyr Ile Val			
	420	425	430
Leu Pro Ile Ser Glu Thr Leu Ser Met Glu Glu Asp Ser Gly Leu Ser			
	435	440	445
Leu Pro Thr Ser Pro Val Ser Cys Met Glu Glu Glu Glu Val Cys Asp			
	450	455	460
Pro Lys Phe His Tyr Asp Asn Thr Ala Gly Ile Ser Gln Tyr Leu Gln			
	465	470	475
Asn Ser Lys Arg Lys Ser Arg Pro Val Ser Val Lys Thr Phe Glu Asp			
	485	490	495
Ile Pro Leu Glu Glu Pro Glu Val Lys Val Ile Pro Asp Asp Asn Gln			
	500	505	510
Thr Asp Ser Gly Met Val Leu Ala Ser Glu Glu Leu Lys Thr Leu Glu			
	515	520	525
Asp Arg Thr Lys Leu Ser Pro Ser Phe Gly Gly Met Val Pro Ser Lys			
	530	535	540
Ser Arg Glu Ser Val Ala Ser Glu Gly Ser Asn Gln Thr Ser Gly Tyr			
	545	550	555
Gln Ser Gly Tyr His Ser Asp Asp Thr Asp Thr Thr Val Tyr Ser Ser			
	565	570	575
Glu Glu Ala Glu Leu Leu Lys Leu Ile Glu Ile Gly Val Gln Thr Gly			
	580	585	590
Ser Thr Ala Gln Ile Leu Gln Pro Asp Ser Gly Thr Thr Leu Ser Ser			
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Pro Pro Val			
	610		

<210> 26
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 <212> DNA
 <213> Homo Sapiens

<400> 1836

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ctacggacgc ttaagcgggc caatggaggg gaactgaaga caggctactt gtccatcgtc	180
atggatccag atgaactccc attgcatgaa cattgtgaac gactgcctta tgatgccagc	240
aaatgggaat tcccagaga ccggctgaag ctaggtaaga ctcttgccg ttggtgcctt	300
ggccaagtga ttgaagcaga tgcctttgga attgacaaga cagcaacttg caggacagta	360
gcagtcacaa tgttgaaaga aggagcaaca cacagtgcgc atcgagctct catgtctgaa	420
ctcaagatcc tcatctat attggtcaccat ctcaatgtgg tcaacctctt aggtgcctgt	480
accaagccag gagggccact catgggtgatt gtggaattct gcaaatcttg aaacctgtcc	540
acttacctga ggagcaagag aaatgaattt gtcccttaca agaccaaaag ggcacgattc	600
cgtcaaggga aagactacgt tggagcaatc cctgtggatc tgaaacggcg cttggacagc	660
atcaccagta gccagagctc agccagctct ggatttgtgg aggagaagtc cctcagtgat	720
gtagaagaag aggaagctcc tgaagatctg tataaggact tctgacctt ggagcatctc	780
atctgttaca gcttcaagt ggctaagggc atggagtctt tggcatcgcg aaagtgtatc	840
cacagggacc tggcggcagc aaatatcttc ttatcggaga agaactgggt taaaatctgt	900
gactttggct tggcccgga tatttataaa gatccagatt atgtcagaaa aggagatgct	960
cgcctccctt tgaaatggat ggcccagaaa acaatttttg acagagtgtc cacaatccag	1020
agtgcagctc ggtcttttgg tgttttgcgt tgggaaatat ttctcttagg tgcttctcca	1080
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